

**IN THE CLAIMS:**

Please cancel claims 1-5 and 9 without prejudice or disclaimer, amend claims 6-8, and add new claims 10-11 as follows:

1-5. (Cancelled)

6. (Currently Amended) A method for ~~deciding~~ determining a base sequence of a primer comprising: ~~providing~~

carrying out a PCR by using four types of primers which, respectively, have a structure comprising a first sequence of a given base length complementary to one of single strands of a target DNA and a second sequence of a given base length non-complementary to said one single strand provided adjacent to the side of 5' terminus of said first sequence and being non-complementary to the one of single strands of the target DNA; which, respectively have, at 5' terminus of said second sequence, one base whose types differ from one another, carrying out PCR by use of the four types of primers;

analyzing the results of amplified products obtained by the PCR to obtain;  
requiring efficiencies of adenylation using results of the step of analyzing;  
thereof; and

determining one out of the four types of primers deciding said second sequence as a sequence which is most likely to undergo adenylation, wherein each of the four types of primers have one base at 5' terminus of the second sequence, the one base being different among the four types of primers.

7. (Currently Amended) A method for ~~deciding~~ determining a base sequence of a primer according to Claim 6, further comprising:

carrying out a second PCR by using another which comprises selecting one base at the 5' terminus of said second sequence, providing four types of primers which, respectively, have the one base shifted from at the 5' terminus by one base toward the side of 3' terminus and individual bases differ in type from one another, carrying out PCR by use of the four types of primers, of the second sequence of the sequence determined in the step of determining one out of the four types of primers, and have a second base located at a second site from the 5' terminus thereof and

different among the another four types of primers;

analyzing the second results of amplified products by the second PCR to determine;

requiring efficiencies of adenylation using results of the step of analyzing the second results; and, from which the one base shifted from the 5' terminus by one base toward the 3' terminus is decided, optionally further providing four types of primers wherein the types of bases differ from each other with respect to one base shifted further by one base toward the 3' terminus and carrying out PCR the last mentioned four types of primers, analyzing the results of amplified product by the last mentioned PCR to obtain efficiencies of adenylation, and successively deciding said second sequence as one which is

determining one out of the another four types of primers to be most likely to undergo adenylation.

8. (Currently Amended) A method for deciding determining a base sequence of a primer comprising; which comprises providing

storing data of anchor sequences whose adenylation efficiencies are preliminarily calculated based upon results of a PCR by using four types of primers which, respectively, have a structure comprising a first sequence of a given base length complementary to one of single strands of a target DNA and a second an anchor sequence of a given base length non-complementary to said one single strand provided adjacent to the side of 5' terminus of said first sequence and being non-complementary to one single strands of the target DNA; and which, respectively have, at 5' terminus of said second sequence, one base whose types differ from one another, carrying out PCR by use of the four types of primers, analyzing the results of amplified product obtained by the PCR to determine said second sequence as a sequence that is most likely to undergo adenylation whereby a second sequence that is most likely to undergo adenylation is preliminarily prepared, and checking, when target DNA is provided, whether or not a primer composed of a combination of the first sequence of a given base length complementary to one of single strands of said target DNA and the preliminarily prepared second sequence has a stable secondary structure.

inputting a sequence of the target DNA;

determining an amplification area in the target DNA;  
designing a forward primer and a reverse primer corresponding to the  
amplification;  
extracting the anchor sequence from the data stored in the step of storing data;  
designing an anchored reverse primer by adding the anchor sequence and the  
reverse primer; and  
calculating probabilities of a secondary structure formation between/inside the  
forward primer and the reverse primer and the anchored reverse primer.

9. (Cancelled)

10. (New) A method for determining a base sequence of a primer according to Claim 7, further comprising steps of

carrying out a third PCR by using other four types of primers which respectively have the one base at the 5' terminus of the second sequence of the sequence determined in the step of determining one out of the another four types of primers, and have a third base located at a third site from the 5' terminus thereof and different among the other four types of primers;

analyzing third results of amplified products obtained by the third PCR;

requiring efficiencies of adenylation using results of the step of analyzing the third results; and

determining one out of the other four types of primers to be most likely to undergo adenylation.

11. (New) A method for making primers comprising:

carrying out a PCR by using four types of primers which respectively have a first sequence of a given base length complementary to one of single strands of a target DNA and a second sequence of a given base length provided adjacent to the side of 5' terminus of the first sequence and being non-complementary to the one of single strands of the target DNA;

analyzing results of amplified products obtained by the PCR;

requiring efficiencies of adenylation using results of the step of analyzing;

determining one out of the four types of primers as a primer sequence which is most likely to undergo adenylation; and

synthesizing primers having the primer sequence determined in the step of determining one out of the four types of primers, wherein each of the four types of primers have one base at 5' terminus of the second sequence, the one base being different among the four types of primers.